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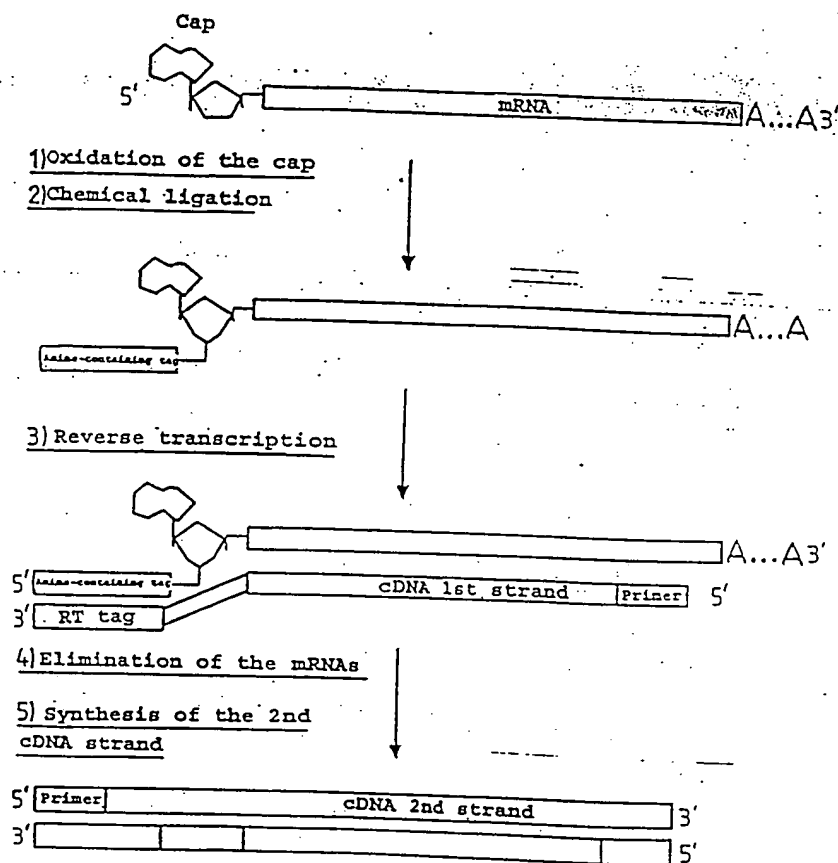


FIGURE 1

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Minimum signal peptide score	false positive rate	false negative rate	proba(0.1)	proba(0.2)
3.5	0,121	0,036	0,467	0,664
4	0,096	0,06	0,618	0,708
4.5	0,078	0,079	0,665	0,745
5	0,062	0,098	0,616	0,782
5.5	0,05	0,127	0,659	0,813
6	0,04	0,163	0,684	0,836
6.5	0,033	0,202	0,725	0,855
7	0,025	0,248	0,763	0,878
7.5	0,021	0,304	0,78	0,889
8	0,015	0,368	0,816	0,909
8.5	0,012	0,418	0,836	0,92
9	0,009	0,512	0,856	0,93
9.5	0,007	0,581	0,863	0,934
10	0,006	0,678	0,835	0,918

FIGURE 2

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Score curves

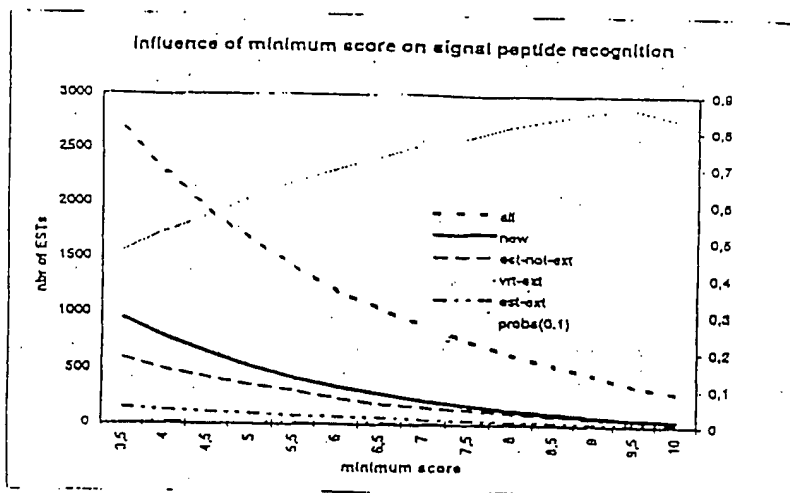


FIGURE 3

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Minimum signal peptide score	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
3,5	2874	947	599	23	150
4	2278	784	489	23	126
4,5	1943	647	425	22	112
5	1657	523	353	21	96
5,5	1417	418	307	19	80
6	1180	340	238	18	68
6,5	1035	280	186	18	60
7	893	219	161	15	48
7,5	753	173	132	12	36
8	636	133	101	11	29
8,5	543	104	83	8	26
9	456	81	63	6	24
9,5	364	57	48	6	18
10	303	47	35	6	15

FIGURE 4

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Tissue	All ESTs	New ESTs	ESTs matching public EST closer than 40 bp from beginning	ESTs extending known mRNA more than 40 bp	ESTs extending public EST more than 40 bp
Brain	329	131	75	3	24
Cancerous prostate	134	40	37	1	6
Cerebellum	17	9	1	0	6
Colon	21	11	4	0	0
Dystrophic muscle	41	18	8	0	1
Fetal brain	70	37	18	0	1
Fetal kidney	227	116	46	1	19
Fetal liver	13	7	2	0	0
Heart	30	15	7	0	1
Hypertrophic prostate	86	23	22	2	2
Kidney	10	7	3	0	0
Large intestine	21	8	4	0	1
Liver	23	9	6	0	0
Lung	24	12	4	0	1
Lung (cells)	57	38	6	0	4
Lymph ganglia	163	60	23	2	12
Lymphocytes	23	6	4	0	2
Muscle	33	16	6	0	4
Normal prostate	181	61	45	7	11
Ovary	90	57	12	1	2
Pancreas	48	11	6	0	1
Placenta	24	5	1	0	0
Prostate	34	16	4	0	2
Spleen	56	28	10	0	1
Substantia nigra	108	47	27	1	6
Suprarenals	15	3	3	1	0
Testis	131	68	25	1	8
Thyroid	17	8	2	0	2
Umbilical cord	65	17	12	1	3
Uterus	28	15	3	0	2
Non tissue-specific	568	48	177	2	28
Total	2577	947	601	23	150

FIGURE 5

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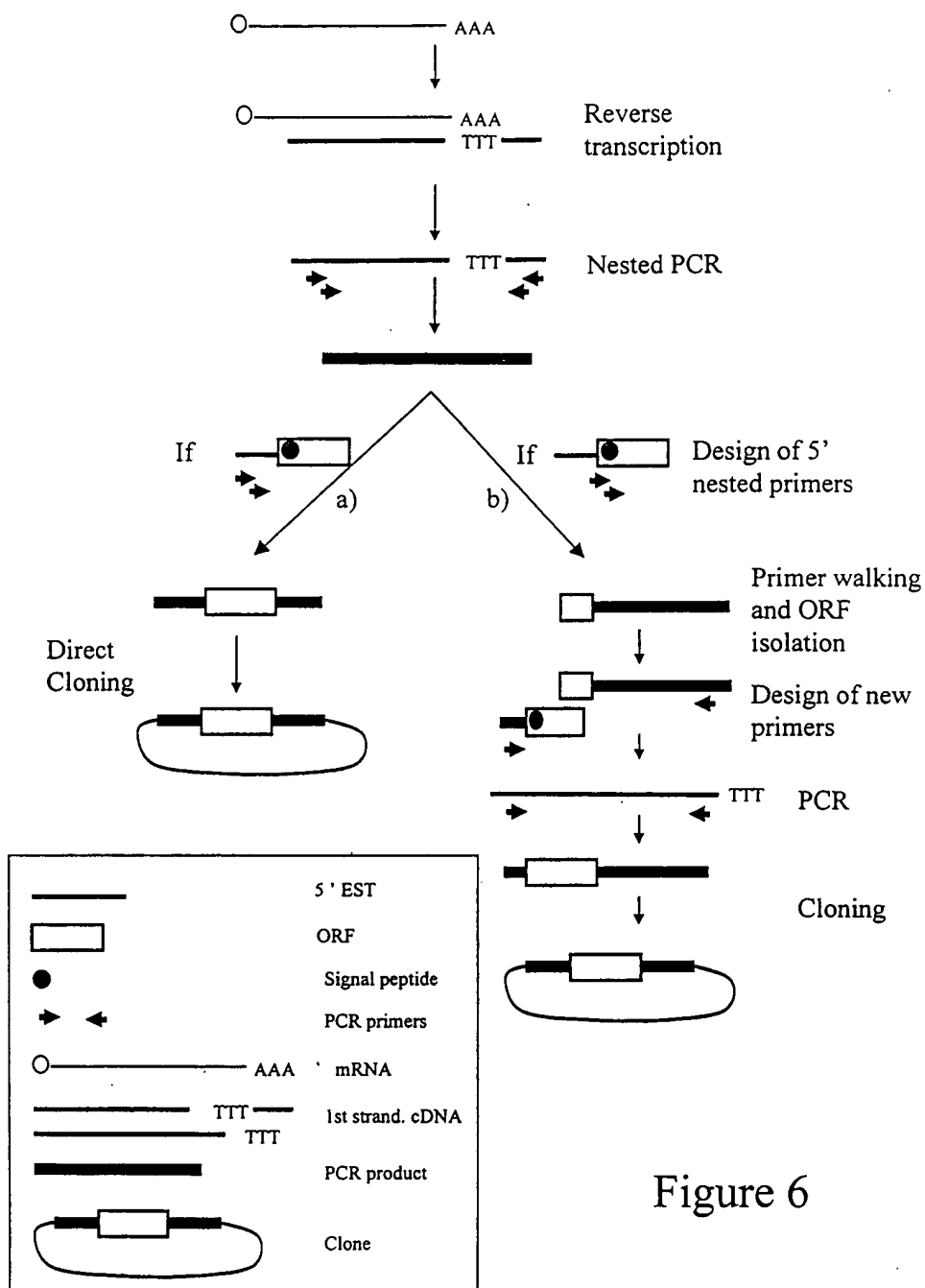
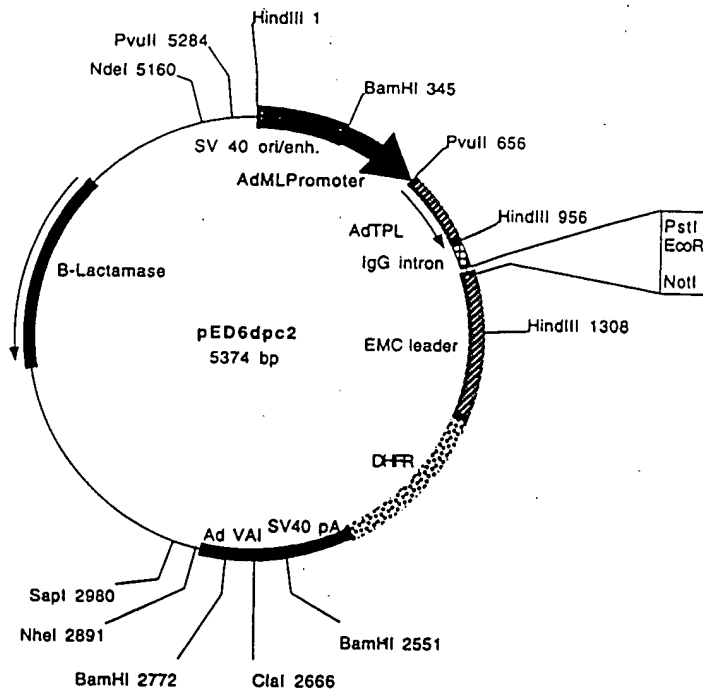


Figure 6

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Plasmid name: pED6dpc2
Plasmid size: 5374 bp

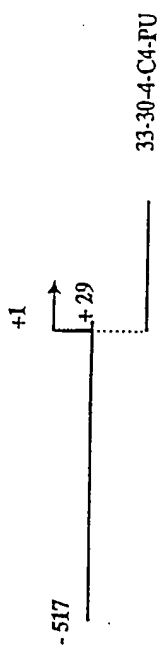
Comments/References: pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 7

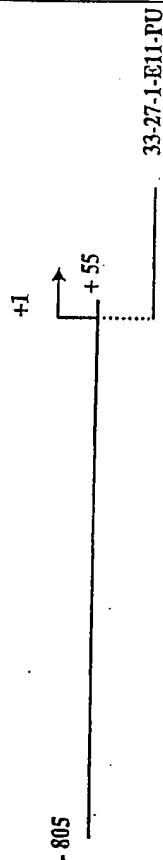
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Description of Promoter structure isolated from SignalTag 5'ESTs

Promoter P13H2



Promoter P15B4



Promoter P29B6

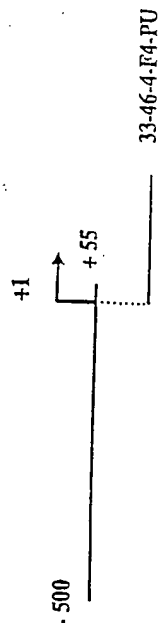


FIGURE 8

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Description of Transcription Factor Binding Sites present on promoters isolated from SignalTag sequences.

Promoter sequence P13H2 (548 bp):

Matrix	Position	Orientation	Score	Length	Sequence
CMYB_01	-502	+	0.963	9	TGTCAGTTG
MYOQ_08	-501	-	0.961	10	CCCAACTGAC
S8_01	-444	-	0.960	11	AATAGAAATTAG
S8_01	-425	-	0.966	11	AAGTAAATTAG
DELTAEF1_01	-390	-	0.960	11	GCACACCTCAG
GATA_C	-384	-	0.964	11	AGATAAATCCA
CMYB_01	-349	+	0.958	9	CTTCAGTTG
GATA1_02	-343	+	0.960	14	TTGTAGATAGGACA
GATA_C	-339	+	0.953	11	AGTAGGACAT
TAL1ALPHA47_01	-235	+	0.973	16	CATAACAGATGGTAAG
TAL1BETA47_01	-235	+	0.963	16	CATAACAGATGGTAAG
TAL1BETA172_01	-235	+	0.978	16	CATAACAGATGGTAAG
MYOQ_08	-232	-	0.954	10	ACCATCTGTT
GATA1_04	-217	-	0.953	13	TCAAGATAAAGTA
IK1_01	-126	+	0.963	18	AGTTGGGAATTC
IK2_01	-126	+	0.965	12	AGTTGGGAATTC
CREL_01	-123	+	0.962	10	TGGGAATTC
GATA1_02	-96	+	0.960	14	TCAGTATATGGCA
SRF_02	-41	-	0.961	12	TAAACAAACA
E2F_02	-33	-	0.957	8	TTTAGCGC
MZF1_01	-6	-	0.976	8	TGAGGGGA

Promoter sequence P16B4 (681 bp):

Matrix	Position	Orientation	Score	Length	Sequence
NFY_Q8	-748	-	0.956	11	GGACCAATCAT
MZF1_01	-738	+	0.962	8	CCTGGGA
CMYB_01	-684	+	0.994	9	TGACCGTTG
MYOQ_02	-682	-	0.965	9	TCCAACGGT
STAT_01	-673	+	0.966	9	TTCCAGAA
STAT_01	-673	-	0.951	9	TTCCAGAA
MZF1_01	-656	-	0.956	8	TTGGGGGA
IK2_01	-451	+	0.965	12	GAATGGGAATTC
MZF1_01	-424	+	0.968	8	AGAGGGGA
SRF_02	-388	-	0.955	12	GAACAAACA
MZF1_01	-216	+	0.960	8	GAAGGGGA
MYOQ_08	-190	+	0.961	10	AGCATCTGCC
DELTAEF1_01	-176	+	0.958	11	TCCCACTTCC
S8_01	6	-	0.992	11	GAGGCAATTAT
MZF1_01	16	-	0.966	8	AGAGGGGA

Promoter sequence P29B6 (555 bp):

Matrix	Position	Orientation	Score	Length	Sequence
ARNT_01	-311	+	0.964	16	GGACTCAGTGTGCT
NMYC_01	-309	+	0.995	12	ACTCAGTGTGCTG
USF_01	-309	+	0.985	12	ACTCAGTGTGCTG
USF_01	-309	-	0.985	12	GAAGCAAGTGAAT
NMYC_01	-309	-	0.956	12	GAAGCAAGTGAAT
MYCHAX_02	-309	-	0.972	12	CAGCAAGTGAAT
USF_C	-307	+	0.997	8	TCAAGTGC
USF_C	-307	-	0.991	8	GCAAGTGA
MZF1_01	-292	-	0.968	8	CATGGGGA
ELK1_02	-105	+	0.963	14	CTCTCCGAAGCCT
CEB1P64_01	-102	+	0.974	10	TCCGGAAGCC
AP1_Q4	-42	-	0.963	11	AGTGAAGTGAAC
AP1FJ_02	-42	-	0.961	11	AGTGAAGTGAAC
PAD6_C	45	+	1.000	9	TGTGGTCTC

Figure 9

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100.0% identity in 125 aa overlap

	10	20	30	40	50	60
SEQ ID NO: 217	MADEEELEALRRQRLAELQAKHGDPGDAAQQEAKHREAEMRNSILAQVLDQSARARLSNLA					
	X::					
SEQ ID NO: 516	MADEEELEALRRQRLAELQAKHGDPGDAAQQEAKHREAEMRNSILAQVLDQSARARLSNLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
SEQ ID NO: 217	LVKPEKTKAVENYLIQMARYGQLSEKVSEQGLIEILKKVSQQTEKTTTVKFNRRKVMDS					
	::					
SEQ ID NO: 516	LVKPEKTKAVENYLIQMARYGQLSEKVSEQGLIEILKKVSQQTEKTTTVKFNRRKVMDS					
	70	80	90	100	110	120

SEQ ID NO: 217 EDDDY

::::X

SEQ ID NO: 516 EDDDY

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FIGURE 10

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CLUSTAL W(1.5) multiple sequence alignment

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SEQ ID NO: 517      MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLS
SEQ ID NO: 232      -----MGCVFQSTEDKCIFKIDWTLS
SEQ ID NO: 174      -----MGCVFQSTEDKRIFKIDWTLS
SEQ ID NO: 175      -----MGCVFQSTVDKCIFKIDWTLS
                      ***** ** *****

SEQ ID NO: 517      PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDNLCNDGSLLLQDVQDVE-----
SEQ ID NO: 232      PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGYICEIRL
SEQ ID NO: 174      PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDNLCNDGSLLLQDVQEQADQGYICEIRL
SEQ ID NO: 175      PGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEQADQGYICEIRL
                      *****

SEQ ID NO: 517      -----
SEQ ID NO: 232      KGESQVFKKAVVLHVLPEEPKGTQMLT-----
SEQ ID NO: 174      KGESQVFKKAVVLHVLPEEPKELMVHVGGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEE
SEQ ID NO: 175      KGESQVFKKAVVLHVLPEEPKELMVHVGGGLIQMGCVFQSTEVKHVTKVEWIFSGR--RAK

SEQ ID NO: 517      -----
SEQ ID NO: 232      -----
SEQ ID NO: 174      IVFRYYHKLMSAEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGN
SEQ ID NO: 175      VTRRKHHCVREGSG-----

SEQ ID NO: 517      -----
SEQ ID NO: 232      -----
SEQ ID NO: 174      LVFKKTIVLHVSPEEPRTLVT PAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCTC
SEQ ID NO: 175      -----

SEQ ID NO: 517      -----
SEQ ID NO: 232      -----
SEQ ID NO: 174      GNKSSVNSTVLVKNTKKTNP
SEQ ID NO: 175      -----

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FIGURE 11

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99.6% identity in 225 aa overlap

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      10      20      30      40      50      60
SEQ ID NO: 515 PTAVQKEEARQDVEALLSRTVTRTQILTGKELRVATQEKEGSSGRCLMTLLGLSFILAGLI
                :
SEQ ID NO: 231                LRVATQEKEGSSGRCLMTLLGLSFILAGLI
                        10      20      30

      70      80      90      100     110     120
SEQ ID NO: 515 VGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAIIDV
                :
SEQ ID NO: 231 VGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAIIDV
                40      50      60      70      80      90

     130     140     150     160     170     180
SEQ ID NO: 515 PVPSFSDSDPAAIHDFEKGMTAYLDLLGNCYLMPNTSIVMPPKNLVELFGKLASGRY
                :
SEQ ID NO: 231 PVPSFSDSDPAAIHDFEKGMTAYLDLLGICYLMPNTSIVMPPKNLVELFGKLASGRY
                100     110     120     130     140     150

     190     200     210     220     230     240
SEQ ID NO: 515 LPQTYVVREDLVAVEEIRDVSNLGIYQLCNRKSFRLRRRDLLGFKRAIDKCWKIR
                :
SEQ ID NO: 231 LPQTYVVREDLVAVEEIRDVSNLGIYQLCNRKSFRLRRRDLLGFKRAIDKCWKIR
                160     170     180     190     200     210

     250     260
SEQ ID NO: 515 HFPNEFIVETKICQE
                :
SEQ ID NO: 231 HFPNEFIVETKICQE
                220
```

FIGURE 12

SEQ ID NO:	196	20	30	40	50	60	70	80	90
SEQ ID NO:196	MERGLKSADPRDGTGYTGWAGIAVLYLHLY								
SEQ ID NO:518	LAEGYFDAAGRLTPEFSQRLTNKIRELLQMERGLKSADPRDGTGYTGWAGIAVLYLHLY								
SEQ ID NO:196	DVFGDPAYLQLAHGYVKQSLNCLTKRSITFLCGDAGPLAVA								
SEQ ID NO:518	DVFGDPAYLQLAHGYVKQSLNCLTKRSITFLCGDAGPLAVA								
SEQ ID NO:196	LIHLNKIDPHAPNEMLYGRIGYIYALLFVNKNFNGVEKTPQSHIQQICETILTSGENLARK								
SEQ ID NO:518	LIHLNKIDPHAPNEMLYGRIGYIYALLFVNKNFNGVEKIPQSHIQQICETILTSGENLARK								
SEQ ID NO:196	RNFTAKSPLMYEWYQEYYVGAHGLAGIYYLMPQSLQVSGQKLHSLVKPSVDYVCQLKF								
SEQ ID NO:518	RNFTAKSPLMYEWYQEYYVGAHGLAGIYYLMPQSLQVSGQKLHSLVKPSVDYVCQLKF								
SEQ ID NO:196	PSGNYPFCIGDNRDLLVHWHGAPGVIYMLIQAYKVFREEEKYLCDA								
SEQ ID NO:518	PSGNYPFCIGDNRDLLVHWHGAPGVIYMLIQAYKVFREEEKYLCDA								
SEQ ID NO:196	KGYGLCHGSAGNAYAFLTLYNLTQDMKYLYRACKFAEWCLEYGEHGCRTPDTPFSLFEGM								
SEQ ID NO:518	KGYGLCHGSAGNAYAFLTLYNLTQDMKYLYRACKFAEWCLEYGEHGCRTPDTPFSLFEGM								
SEQ ID NO:196	AGTIYFLADLLVPTKARFPFEL								
SEQ ID NO:518	AGTIYFLADLLVPTKARFPFEL								

FIGURE 13

98.5% identity in 194 aa overlap

	90	100	110	120	130	140
SEQ ID NO:519	ARNLPPLTDAQKNKLRHLSVVTLAAKVKCI PYAVLLEALALRNVRQLEDLVIEAVYADVL					
	::					
SEQ ID NO:158	ARNLPPLTEAQKNKLRHLSVVTLAAKVKCI PYAVLLEALALRNVRQLEDLVIEAVYADVL					
	60	70	80	90	100	110

	150	160	170	180	190	200
SEQ ID NO:519	RGS LDQRNQRLEVDYSIGRDIQRQDLSAIAQTLQEWCVGCEVVLSGIEEQVSRANQHKEQ					
	::					
SEQ ID NO:158	RGS LDQRNQRLEVDYSIGRDIQRQDLSAIAQTLQEWCVGCEVVLSGIEEQVSRANQHKEQ					
	120	130	140	150	160	170

	210	220	230	240	250	260
SEQ ID NO:519	QLGLKQQIESEVANLKKTIKVT TAAAAAATSQDPEQHLTELREPASGTNQRQPSKKASKG					
	::					
SEQ ID NO:158	QLGLKQQIESEVANLKKTIKVT TAAAAAATSQDPEQHLTELREPAPGTNQRQPSKKASKG					
	180	190	200	210	220	230

	270
SEQ ID NO:519	KGLRGS AKIWSKSN
	::::::::::::
SEQ ID NO:158	KGLRGS AKIWSKSN
	240 250

88.7% identity in 62 aa overlap

	10	20	30	40	50	60
SEQ ID NO:519	MSAEVKVTGQNQEQLLLAKSAKGAALATLIHQVLEAPGVYVFGELLDMPNVRELAESDF					
	::					
SEQ ID NO:158	MSAEVKVTGQNQEQLLLAKSAKGAALATLIHQVLEAPGVYVFGELLDMPNVRELXARNL					
	10	20	30	40	50	60

SEQ ID NO:519 AS
.X
SEQ ID NO:158 PP

FIGURE 14

		10	20	30	40	50	
SEQ ID NO:226	MIARRNPVPLRFLPDEARSLPPPKLTDPRLLYIGFLGYCSGLIDNLIARRRPIATAGLHR						
						
SEQ ID NO:514	MMTRQGRATFQFLPDEARSLPPPKLTDPRLAFVGLGYCSGLIDNAIRRRPVLLAGLHR						
		10	20	30	40	50	60
		60	70				
SEQ ID NO:226	QLLYITAFFLLDIIL						
						
SEQ ID NO:514	QLLYITSFVFGVYLLKRQDYMAYVRDHDMFSYIKSHPEDFPEKDKKTYGEVFEEFHPVR						
		70	80	90	100	110	120

FIGURE 15